



Applicant: Soto, et al.
USSN: 09/512,581

APPENDIX A

TABLE 1. CLUSTALW alignment of SEQ ID NO: 2 ("SID2") and murine AS3 polypeptide (mAS3) as disclosed in GenBank Accession No. AY102267.

SID2:	1	MAHSKTRTNDGKITYPGVEISDKISKEEMVRRLLKMVVKTFMDMDQDSEEEKELYLNLA	60
MAS3:	1	MAHSKTRTNDGKITYPGVEISDKISKEEMVRRLLKMVVKTFMDMDQDSEEEKELYLNLA	60
SID2:	61	LHLASDFFLKHPGKDVRLLVACCLADIFRIYAPEAPYTSDPKLDKDFMFITRQLKGLED	120
MAS3:	61	LHLASDFFLKHPKDVRLLVACCLADIFRIYAPEAPYTSDPKLDKDFMFITRQLKGLED	120
SID2:	121	KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL	180
MAS3:	121	KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL	180
SID2:	181	MSSIIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIIEPYITFFNQV	240
MAS3:	181	MSSIIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIIEPYITFFNQV	240
SID2:	241	LMLGKTSISDLSEHVFDLILELYNIDSHLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF	300
MAS3:	241	LMLGKTSISDLSEHVFDLILELYNIDSHLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF	300
SID2:	301	GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHDPDLAKDLTEYLKVRSH	360
MAS3:	301	GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHDPDLAKDLTEYLKVRSH	360
SID2:	361	DPEEAIKRDVIVSIVTAAKDKILLVNDHLLNFVRERTLDKRWVRKEAMMGLAQIYKKYA	420
MAS3:	361	DPEEAIKRDVIVSIVTAAKDKILLVNDHLLNFVRERTLDKRWVRKEAMMGLAQIYKKY+	420
SID2:	421	LQSAAGKDAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMCKLYYL	480
MAS3:	421	LQSAAGKDAKQISWVKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMCKLYYL	480
SID2:	481	YATLDLNAVKALEKQNLRLRHQVKDLDLQPKTDASVKAIFSKVMVITRNLDPDG	540
MAS3:	481	YATLDLNAVKALEKQNLRLRHQVKDLDLQPKTDASVKAIFSKVMVITRNLDPDG	540
SID2:	541	KAQDFMCKFTQVLEDDKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM	600
MAS3:	541	KAQDFMCKFTQVLEDDKIRKQLEALVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM	600
SID2:	601	IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH	660
MAS3:	601	IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH	660
SID2:	661	PISFHSIAETFESLLACLKMDDEKVAEALQIFKNTGSKIEEDFPHIRSALLPVLHHSKK	720
MAS3:	661	PISFHSIAETFESLLACLKMDDEKVAEALQIFKNTGSKIEEDFPHIRSALLPVLHHSKK	720
SID2:	721	GPPRQAKYAIHCHIAIFSSKETQFAQIFEPLHKSLEDPNLEHLITPLVTIGHIALLAPDQ	780
MAS3:	721	GPPRQAKYAIHCHIAIFSSKETQFAQIFEPLHKSLEDPNLEHLITPLVTIGHIALLAPDQ	780
SID2:	781	FAAPWKSIVATFIVKDLLMNDRLPGKKTTLKLVVPDEEVSPETMVKIQAIKMMVRWLLGMK	840
MAS3:	781	FAAPLKSIVATFIVKDLLMNDRLPGKKTTLKLVVPDEEVSPETMVKIQAIKMMVRWLLGMK	840

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SID2: 841 NNHKSSTLRLTTILHSDGDLTEQGIKSKPDMSRLRLAAGSAIVKLAQEPYHEIIT 900
NNHKSSTLRLTTILHSDGDLTEQGIKSKPDMSRLRLAAGSAIVKLAQEPYHEIIT
MAS3: 841 NNHKSSTLRLTTILHSDGDLTEQGIKSKPDMSRLRLAAGSAIVKLAQEPYHEIIT 900

SID2: 901 LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRPLEYMAICALCAKDPVKERRAHARQ 960
LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRPLEYMAICALCAKDPVKERRAHARQ
MAS3: 901 LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRPLEYMAICALCAKDPVKERRAHARQ 960

SID2: 961 CLVKNINVRREYLKQHAHVSEKLLSLLPEYVVPYTIHLLAHPDYVKVDIEQLKDVKEC 1020
CLVKN VRREYLKQHA+VSEKLLSLLPEYVVPYTIHLLAHPDYVKVDIEQLKDVKEC
MAS3: 961 CLVKNITVRREYLKQHASVSEKLLSLLPEYVVPYTIHLLAHPDYVKVDIEQLKDVKEC 1020

SID2: 1021 LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDDAKMNEKLYTVC DVAMNIIMSKS 1080
LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDD KMNEKLYTVC DVAMNIIMSKS
MAS3: 1021 LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDDTKMNEKLYTVC DVAMNIIMSKS 1080

SID2: 1081 TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTTNVLGAVNKPLSS 1140
TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKT NVLGAVNKPLSS
MAS3: 1081 TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTANVLGAVNKPLSS 1140

SID2: 1141 AGKQSQTSSRMETVSNASSSSNPSSPGRIKGRDSSSEMDHSENEYTMSSPLPGKKSDK 1200
AGKQSQTSSRMETVSNASSSSNPSSPGRIKGRDSSSEMDHSENEYTMSSPLPGKKSDK
MAS3: 1141 AGKQSQTSSRMETVSNASSSSNPSSPGRIKGRDSSSEMDHSENEYTMSSPLPGKKSDK 1200

SID2: 1201 RDDSDLVRSELEKPRGRKKTPTVTEQEEKLGMDDLTKLVQEQKPKGSQSRKRGHTASESD 1260
R+D DL SELEKPR RKK PVT+ EEKLGMDDLTKLVQEQKPKGSQR RKRGTAS+SD
MAS3: 1201 REDPDL--SELEKPRSRKKAPVTDPEEKLGMDDLTKLVQEQKPKGSQGRKRGRTASDSD 1258

SID2: 1261 EQQWPEEKRLKEDIENEDEQNSPPKKGKRGRPPKPLGGGTPKEEPTMKTSKKGSKKKSG 1320
EQQWPEEKR KE++LENEDEQNSPPKKGKRGRPPKPLGGGT KEEPTMKTSKKG+KKK
MAS3: 1259 EQQWPEEKRHKEELLENEDEQNSPPKKGKRGRPPKPLGGGTSKEEPTMKTSKKGNKKKL 1318

SID2: 1321 PPAPEEEEEERQSGNTEQSKSKQHRVSRRAQRAESPESAIESTQSTPQKGRGRPSK 1380
PP +++EEERQ GNTE KSKSKQHR S+RAQRAESPE+SA+ESTQSTPQKGRGRPSK
MAS3: 1319 PPVVDDDEEERQIGNTEHKSQHRVSRRAQRAESPESAIESTQSTPQKGRGRPSK 1378

SID2: 1381 TPSPSQPKKNV 1391
PSPSQP K +
MAS3: 1379 APSPSQPPKKI 1389

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